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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/930,906

DATE: 08/23/2001
TIME: 16:50:38

Input Set : A:\2363921.app
Output Set: N:\CRF3\08162001\I930906.raw

3 <110> APPLICANT: Tarczynski, Mitchell C
 4 Li, Changjiang
 6 <120> TITLE OF INVENTION: Methods and Compositions for Modifying Oil and Protein
 7 Content in Plants
 9 <130> FILE REFERENCE: 5718-113 (35718/236392)
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/930,906
 C--> 12 <141> CURRENT FILING DATE: 2001-08-16
 14 <150> PRIOR APPLICATION NUMBER: 60/226,142
 15 <151> PRIOR FILING DATE: 2000-08-18
 17 <160> NUMBER OF SEQ ID NOS: 6
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 2245
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Zea mays
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (138)..(1844)
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 35 gagcacgggg acatcaa atg gcg gca gcg gcg gag atc ggt ggt ttc gcg 170
 36 Met Ala Ala Ala Ala Glu Ile Gly Gly Phe Ala
 37 1 5 10
 39 gcg gcg aga gtg gcg gtg gca acg ctc agg ccg gct gcg cac cca gcc 218
 40 Ala Ala Arg Val Ala Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala
 41 15 20 25
 43 ccg gcg gcg gcg gca ccg cag cct agg agg gcg gtg gcg gcg cag 266
 44 Pro Ala Ala Ala Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln
 45 30 35 40
 47 tcg ctg cag acg acc gcc acc gag gcg ctg acg gcg gat ctc gcc ggc 314
 48 Ser Leu Gln Thr Thr Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly
 49 45 50 55
 51 acg acc aac ggc gct gtg cat gct cgg atg aat agt aag gct aca agt 362
 52 Thr Thr Asn Gly Ala Val His Ala Arg Met Asn Ser Lys Ala Thr Ser
 53 60 65 70 75
 55 gaa atc act tca cag gca gtt act gca aat tct agg aga aag aca aag 410
 56 Glu Ile Thr Ser Gln Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys
 57 80 85 90
 59 ata gtc tgc acc ata ggt ccc tca acc aac act cgt gag atg att tgg 458
 60 Ile Val Cys Thr Ile Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp
 61 95 100 105
 63 aag ctt gca gag act gga atg aat gta gcg cgc ctt aat atg tcc cat 506
 64 Lys Leu Ala Glu Thr Gly Met Asn Val Ala Arg Leu Asn Met Ser His
 65 110 115 120
 67 ggt gac cac cag tcg cac cag aag gtt att gat ttg gtc aag gag tac
 68 Gly Asp His Gln Ser His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr

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69	125	130	135	
71	aat gca cag aac act gat ggc aat gtt att gcc att atg ctg gac aca			602
72	Asn Ala Gln Asn Thr Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr			
73	140	145	150	155
75	aag ggt cct gaa gtt aga agt ggg gat gtt cca gag cca atc atg ctc			650
76	Lys Gly Pro Glu Val Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu			
77	160	165	170	
79	aag gaa ggt caa gag ttc aac ttc acg att aaa aga ggg gtg agc act			698
80	Lys Glu Gly Gln Glu Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr			
81	175	180	185	
83	gaa gac act gtc agc gtc aac tat gat gac ttc ata aat gat gtt gaa			746
84	Glu Asp Thr Val Ser Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu			
85	190	195	200	
87	gct ggc gac ata cta tta gtc gat gga gga atg atg tcg ctt gct gtc			794
88	Ala Gly Asp Ile Leu Leu Val Asp Gly Gly Met Met Ser Leu Ala Val			
89	205	210	215	
91	aag tct aaa aca gcc gat aca gtc aag tgt aaa gta gtt gat ggt ggg			842
92	Lys Ser Lys Thr Ala Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly			
93	220	225	230	235
95	gaa ttg aaa tca cgg cgc cac cta aat gtc cgt gga aag agt gct act			890
96	Glu Leu Lys Ser Arg Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr			
97	240	245	250	.
99	ttg cca tct atc act gag aag gat tgg gaa gac ata aaa ttt ggt gtc			938
100	Leu Pro Ser Ile Thr Glu Lys Asp Trp Glu Asp Ile Lys Phe Gly Val			
101	255	260	265	
103	gaa aac ggt gtt gat ttc tat gca gtt tcc ttt gtc aag gat gcc aaa			986
104	Glu Asn Gly Val Asp Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys			
105	270	275	280	
107	gtt atc cat gaa tta aaa gac tac ctt aaa agt gct aat gcc gat ata			1034
108	Val Ile His Glu Leu Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile			
109	285	290	295	
111	cat gtc att cca aaa att gaa agt gca gat tca ata cca aac ctg cag			1082
112	His Val Ile Pro Lys Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln			
113	300	305	310	315
115	tcc att att gct gct tca gat ggg gca atg gtc gcg cgt gga gac ctt			1130
116	Ser Ile Ile Ala Ala Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu			
117	320	325	330	
119	ggt gct gaa ctt ccg att gag gat gtt cct ttg cta cag gca gag att			1178
120	Gly Ala Glu Leu Pro Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile			
121	335	340	345	
123	gtc caa aca tgt cga agc atg gag aaa cca gtc att gtc gct aca aat			1226
124	Val Gln Thr Cys Arg Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn			
125	350	355	360	
127	atg ttg gaa agc atg att gac cat cct act ccc act agg gca gaa gtt			1274
128	Met Leu Glu Ser Met Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val			
129	365	370	375	
131	tct gac ata gct att gca gtt cgg gaa ggt gct gat gcc atc atg tta			1322
132	Ser Asp Ile Ala Ile Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu			
133	380	385	390	395

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135 tct ggc gaa act gct cat gga aag tat cca cta aag gca gtc aag gtc 1370
 136 Ser Gly Glu Thr Ala His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val
 137 400 405 410
 139 atg cac act gtg gca ctc aga aca gaa tcc agc ctt tat aac cca act 1418
 140 Met His Thr Val Ala Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr
 141 415 420 425
 143 act tct cct agt ctt gtt gca tct gca cag ggt cta cag aat gag gac 1466
 144 Thr Ser Pro Ser Leu Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp
 145 430 435 440
 147 ttc tcc gca agc cag cta agt aaa atg ttc gga tct cat gca acg atg 1514
 148 Phe Ser Ala Ser Gln Leu Ser Lys Met Phe Gly Ser His Ala Thr Met
 149 445 450 455
 151 atg gcc aac acc ctt cgc aca cca atc att gta ttt aca cag aca ggc 1562
 152 Met Ala Asn Thr Leu Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly
 153 460 465 470 475
 155 tcc atg gct gtc ctc ctg agc cac tat cgt ccc tcg tct aca cta ttt 1610
 156 Ser Met Ala Val Leu Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe
 157 480 485 490
 159 gca ttt aca aac gag gaa cga gtg aag caa cgg cta gca ctc tac cag 1658
 160 Ala Phe Thr Asn Glu Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln
 161 495 500 505
 163 ggc gtc atc cct att cac atg cag ttc tct gac gac gca gaa gaa act 1706
 164 Gly Val Ile Pro Ile His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr
 165 510 515 520
 167 ttc tcc aga gca att agc agc ttg ctg aaa gca caa tat gtg aag aag 1754
 168 Phe Ser Arg Ala Ile Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys
 169 525 530 535
 171 gga gac tac gtc act ctt gtt cag agc gga gtg act tca atc tgg aga 1802
 172 Gly Asp Tyr Val Thr Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg
 173 540 545 550 555
 175 gag gaa tcc act cac cac atc caa gtg agg aaa gtt cag gtc 1844
 176 Glu Glu Ser Thr His His Ile Gln Val Arg Lys Val Gln Val
 177 560 565
 179 tgatgtgccg gtggaaattt gtcgtctgag aaattttgat agccgcct gatgtgttat 1904
 181 catcattata tggtaatatt tactgtttt ccaggagatt gctacgtcga gttatatgtt 1964
 183 gtgtcgaatt cacgtgttagg ctctgaatct tgactgtgtt cgttcatttt cgcttggttc 2024
 185 acactgaagt gttataagct caactttact gctttgttt tcttgtaaaa cttgagttt 2084
 187 gtttcttggc acaaaaggag cttagcactaa caggggtggg agttttgtaa acggggcggag 2144
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 195 <211> LENGTH: 569
 196 <212> TYPE: PRT
 197 <213> ORGANISM: Zea mays
 199 <400> SEQUENCE: 2
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 201 1 5 10 15
 203 Val Ala Thr Leu Arg Pro Ala Ala His Pro Ala Pro Ala Ala Ala
 204 20 25 30

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206 Ala Pro Gln Pro Arg Arg Ala Val Ala Ala Gln Ser Leu Gln Thr Thr
207 35 40 45
209 Ala Thr Glu Ala Leu Thr Ala Asp Leu Ala Gly Thr Thr Asn Gly Ala
210 50 55 60
212 Val His Ala Arg Met Asn Ser Lys Ala Thr Ser Glu Ile Thr Ser Gln
213 65 70 75 80
215 Ala Val Thr Ala Asn Ser Arg Arg Lys Thr Lys Ile Val Cys Thr Ile
216 85 90 95
218 Gly Pro Ser Thr Asn Thr Arg Glu Met Ile Trp Lys Leu Ala Glu Thr
219 100 105 110
221 Gly Met Asn Val Ala Arg Leu Asn Met Ser His Gly Asp His Gln Ser
222 115 120 125
224 His Gln Lys Val Ile Asp Leu Val Lys Glu Tyr Asn Ala Gln Asn Thr
225 130 135 140
227 Asp Gly Asn Val Ile Ala Ile Met Leu Asp Thr Lys Gly Pro Glu Val
228 145 150 155 160
230 Arg Ser Gly Asp Val Pro Glu Pro Ile Met Leu Lys Glu Gly Gln Glu
231 165 170 175
233 Phe Asn Phe Thr Ile Lys Arg Gly Val Ser Thr Glu Asp Thr Val Ser
234 180 185 190
236 Val Asn Tyr Asp Asp Phe Ile Asn Asp Val Glu Ala Gly Asp Ile Leu
237 195 200 205
239 Leu Val Asp Gly Gly Met Met Ser Leu Ala Val Lys Ser Lys Thr Ala
240 210 215 220
242 Asp Thr Val Lys Cys Lys Val Val Asp Gly Gly Glu Leu Lys Ser Arg
243 225 230 235 240
245 Arg His Leu Asn Val Arg Gly Lys Ser Ala Thr Leu Pro Ser Ile Thr
246 245 250 255
248 Glu Lys Asp Trp Glu Asp Ile Lys Phe Gly Val Glu Asn Gly Val Asp
249 260 265 270
251 Phe Tyr Ala Val Ser Phe Val Lys Asp Ala Lys Val Ile His Glu Leu
252 275 280 285
254 Lys Asp Tyr Leu Lys Ser Ala Asn Ala Asp Ile His Val Ile Pro Lys
255 290 295 300
257 Ile Glu Ser Ala Asp Ser Ile Pro Asn Leu Gln Ser Ile Ile Ala Ala
258 305 310 315 320
260 Ser Asp Gly Ala Met Val Ala Arg Gly Asp Leu Gly Ala Glu Leu Pro
261 325 330 335
263 Ile Glu Asp Val Pro Leu Leu Gln Ala Glu Ile Val Gln Thr Cys Arg
264 340 345 350
266 Ser Met Glu Lys Pro Val Ile Val Ala Thr Asn Met Leu Glu Ser Met
267 355 360 365
269 Ile Asp His Pro Thr Pro Thr Arg Ala Glu Val Ser Asp Ile Ala Ile
270 370 375 380
272 Ala Val Arg Glu Gly Ala Asp Ala Ile Met Leu Ser Gly Glu Thr Ala
273 385 390 395 400
275 His Gly Lys Tyr Pro Leu Lys Ala Val Lys Val Met His Thr Val Ala
276 405 410 415
278 Leu Arg Thr Glu Ser Ser Leu Tyr Asn Pro Thr Thr Ser Pro Ser Leu

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279 420 425 430
 281 Val Ala Ser Ala Gln Gly Leu Gln Asn Glu Asp Phe Ser Ala Ser Gln
 282 435 440 445
 284 Leu Ser Lys Met Phe Gly Ser His Ala Thr Met Met Ala Asn Thr Leu
 285 450 455 460
 287 Arg Thr Pro Ile Ile Val Phe Thr Gln Thr Gly Ser Met Ala Val Leu
 288 465 470 475 480
 290 Leu Ser His Tyr Arg Pro Ser Ser Thr Leu Phe Ala Phe Thr Asn Glu
 291 485 490 495
 293 Glu Arg Val Lys Gln Arg Leu Ala Leu Tyr Gln Gly Val Ile Pro Ile
 294 500 505 510
 296 His Met Gln Phe Ser Asp Asp Ala Glu Glu Thr Phe Ser Arg Ala Ile
 297 515 520 525
 299 Ser Ser Leu Leu Lys Ala Gln Tyr Val Lys Lys Gly Asp Tyr Val Thr
 300 530 535 540
 302 Leu Val Gln Ser Gly Val Thr Ser Ile Trp Arg Glu Glu Ser Thr His
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 305 His Ile Gln Val Arg Lys Val Gln Val
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 311 <211> LENGTH: 1922
 312 <212> TYPE: DNA
 313 <213> ORGANISM: Zea mays
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 324 ctctcctttg cttgcgcaga tctagcg atg gcg gcg ggc ggt gag ttg gcg tgg 174
 325 Met Ala Ala Gly Gly Glu Leu Ala Trp
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 328 ggg gag gag ccc gtg gcg cgg cgc cgg cct aag acc aag atc gtc tgc 222
 329 Gly Glu Glu Pro Val Ala Arg Arg Pro Lys Thr Lys Ile Val Cys
 330 10 15 20 25
 332 acg ctc ggc cgc gcg tgc cga tcc gtc gag atg atc tcg cgc ctg ctg 270
 333 Thr Leu Gly Pro Ala Ser Arg Ser Val Glu Met Ile Ser Arg Leu Leu
 334 30 35 40
 336 cgc gcc ggg atg tgc gtc gcg cgc ttc aac ttc tcc cat ggc tcc cac 318
 337 Arg Ala Gly Met Cys Val Ala Arg Phe Asn Phe Ser His Gly Ser His
 338 45 50 55
 340 gag tac cac cag gag acg ctc gac aac ctg cac gcc gcc atg gag ctc 366
 341 Glu Tyr His Gln Glu Thr Leu Asp Asn Leu His Ala Ala Met Glu Leu
 342 60 65 70
 344 acc ggg atc ctc tgc gcc gtt atg ctc gac acc aag ggt cca gag att 414
 345 Thr Gly Ile Leu Cys Ala Val Met Leu Asp Thr Lys Gly Pro Glu Ile
 346 75 80 85
 348 aga act gga ttt ttg aaa gat ggg aag cct att caa ttg ata aaa ggc 462
 349 Arg Thr Gly Phe Leu Lys Asp Gly Lys Pro Ile Gln Leu Ile Lys Gly

VERIFICATION SUMMARY
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Input Set : A:\2363921.app
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date